NO: 11) anneals at the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV RnaseH$^-$) transcribes the antisense strand until it reaches the end of the RNA strand when it adds additional C residues. If a primer (SMII: AAGCAGTGGTAACAACGCAGAGTACGCGGG (SEQ ID NO: 12) or ML2G: AAGTGGCAACAGAGATAACGCGTACGCGGG (SEQ ID NO: 13)) ending with 3 Gs is added, it anneals to the added Cs and the MMLV recognizes the rest of the primer sequence as template and continues transcription. As a result, the synthesized cDNAs contain specific sequence tags at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same sequence (CDS and SMII) it is referred to as "symmetric". When the 5' end is tagged with a different sequence than the 3' end (CDS and ML2G) is referred to as "asymmetric". A double-stranded "cDNA library " is then generated by PCR amplification using the 3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT (Portion of SEQ ID NO: 11) and ML2: AAGTGGCAACAGAGATAACGCGT (Portion of SEQ ID NO: 13)) that anneal to the added sequence tags.

On page 125, delete the first full paragraph, and replace this paragraph with the following in accordance with 37 C.F.R. §1.121. A marked up version showing changes is attached:

In order to prepare a cDNA fragment for production of a ^{32}P labeled probe for SGP061, two oligonucleotides, 5'-TTGCGGAGCTTGACGCGC-3' (SEQ ID NO: 14) and 5'-TCCCATCCTTTGTTGCCCG-3'(SEQ ID NO: 15), were used to amplify a 430 basepair fragment by PCR. The fragment was purified by separation on an agarose gel and the sequence was verified by using the same oligonucleotides as primers for the sequencing reaction. The PCR product was detectable in a range of tissue sources including prostate, placenta, salivary gland, skeletal muscle, spinal cord as well as many tumor cell lines. This cDNA fragment was then used to determine the expression of SGP061 on tissue arrays as described above. Initial comparison of normal tissue expression levels with tumor cell line expression levels revealed that SGP061 was elevated in a number of tumor cell lines including those derived from breast, colon, leukemia, lung, melanoma, glioblastoma, ovarian and renal tissue sources.

On page 136 and bridging page 137, delete the last full paragraph, and replace this paragraph with the following in accordance with 37 C.F.R. §1.121. A marked up version showing changes is attached:

Composition of Buffer

10x PanMix

5% Triton X-100

10% non-fat dry milk (Carnation)

10 mM EGTA

250 mM NaF

250 μg/mL Heparin (sigma)

250 μg/mL sheared, boiled salmon sperm DNA (sigma)

0.05% Na azide

Prepared in PBS

Wash Buffer

PBS supplemented with:

0.5% NP-40

25 μl g/mL heparin

PCR reaction mix

1.0 mL 10x PCR buffer (Perkin-Elmer, with 15 mM Mg)

0.2 mL each dNTPs (10 mM stock)

0.1 mL T7UP primer (15 pmol/μL) GGAGCTGTCGTATTCCAGTC (SEQ ID NO: 16)

0.1 mL T7DN primer (15 pmol/μL) AACCCCTCAAGACCCGTTTAG (SEQ ID NO: 17)

0.2 mL 25 mM $MgCl_2$ or $MgSO_4$ to compensate for EDTA

Q.S. to 10 mL with distilled water

Add 1 unit of Taq polymerase per 50 μL reaction

LIBRARY: T7 Select1-H441